

## SEQUENCE LISTING

SubC1

&lt;110&gt; Fuso Pharmaceutical Industries Ltd.

&lt;120&gt; Novel serine protease BSSP6

5 &lt;130&gt; 661641

&lt;150&gt; JP 10-347802

&lt;151&gt; 1998-11-20

&lt;160&gt; 39

10

&lt;210&gt; 1

&lt;211&gt; 1301

&lt;212&gt; DNA

&lt;213&gt; human

15

&lt;400&gt; 1

ctgccttgct ccacacctgg tcaggggaga gaggggagga aagccaaggg aaggaccta 60

actgaaaaca aacaagctgg gagaagcagg aatctgcgct cgggttcg 109

cag atg cag agg ttg agg tgg ctg cgg gac tgg aag tca tcg ggc aga ggt 160

20 Met Gln Arg Leu Arg Trp Leu Arg Asp Trp Lys Ser Ser Gly Arg Gly

-50

-45

-40

ctc aca gca gcc aag gaa cct ggg gcc cgc tcc tcc ccc ctc cag gcc atg 211

Leu Thr Ala Ala Lys Glu Pro Gly Ala Arg Ser Ser Pro Leu Gln Ala Met

-35

-30

-25

25 agg att ctg cag tta atc ctg ctt gct ctg gca aca ggg ctt gta ggg gga 262

Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu Val Gly Gly  
 -20                      -15                      -10                      -5  
 gag acc agg atc atc aag ggg ttc gag tgc aag cct cac tcc cag ccc tgg 313  
 Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro His Ser Gln Pro Trp  
 5                      -1      1                      5                      10  
 cag gca gcc ctg ttc gag aag acg cgg cta ctc tgt ggg gcg acg ctc atc 364  
 Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly Ala Thr Leu Ile  
 15                      20                      25                      30  
 gcc ccc aga tgg ctc ctg aca gca gcc cac tgc ctc aag ccc cgc tac ata 415  
 10 Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu Lys Pro Arg Tyr Ile  
 35                      40                      45  
 gtt cac ctg ggg cag cac aac ctc cag aag gag gag ggc tgt gag cag acc 466  
 Val His Leu Gly Gln His Asn Leu Gln Lys Glu Glu Gly Cys Glu Gln Thr  
 50                      55                      60                      65  
 15 cgg aca gcc act gag tcc ttc ccc cac ccc ggc ttc aac aac agc ctc ccc 517  
 Arg Thr Ala Thr Glu Ser Phe Pro His Pro Gly Phe Asn Asn Ser Leu Pro  
 70                      75                      80  
 aac aaa gac cac cgc aat gac atc atg ctg gtg aag atg gca tcg cca gtc 568  
 Asn Lys Asp His Arg Asn Asp Ile Met Leu Val Lys Met Ala Ser Pro Val  
 20                      85                      90                      95  
 tcc atc acc tgg gct gtg cga ccc ctc acc ctc tcc tca cgc tgt gtc act 619  
 Ser Ile Thr Trp Ala Val Arg Pro Leu Thr Leu Ser Ser Arg Cys Val Thr  
 100                      105                      110                      115  
 gct ggc acc agc tgc ctc att tcc ggc tgg ggc agc acg tcc agc ccc cag 670  
 25 Ala Gly Thr Ser Cys Leu Ile Ser Gly Trp Gly Ser Thr Ser Ser Pro Gln

	120	125	130	
	tta cgc ctg cct cac acc ttg cga tgc gcc aac atc acc atc att gag cac	721		
	Leu Arg Leu Pro His Thr Leu Arg Cys Ala Asn Ile Thr Ile Ile Glu His			
	135	140	145	150
5	cag aag tgt gag aac gcc tac ccc ggc aac atc aca gac acc atg gtg tgt	772		
	Gln Lys Cys Glu Asn Ala Tyr Pro Gly Asn Ile Thr Asp Thr Met Val Cys			
	155	160	165	
	gcc agc gtg cag gaa ggg ggc aag gac tcc tgc cag ggt gac tcc ggg ggc	823		
	Ala Ser Val Gln Glu Gly Gly Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly			
10	170	175	180	
	cct ctg gtc tgt aac cag tct ctt caa ggc att atc tcc tgg ggc cag gat	874		
	Pro Leu Val Cys Asn Gln Ser Leu Gln Gly Ile Ile Ser Trp Gly Gln Asp			
	185	190	195	200
	ccg tgt gcg atc acc cga aag cct ggt gtc tac acg aaa gtc tgc aaa tat	925		
15	Pro Cys Ala Ile Thr Arg Lys Pro Gly Val Tyr Thr Lys Val Cys Lys Tyr			
	205	210	215	
	gtg gac tgg atc cag gag acg atg aag aac aat tagactggac ccacccacca	978		
	Val Asp Trp Ile Gln Glu Thr Met Lys Asn Asn			
	220	225		
20	cagcccatca cctccattt ccacttggtg tttgggttcct gttcactctg ttaataagaa	1038		
	accctaagcc aagaccctct acgaacattc tttgggcctc ctggactaca ggagatgctg	1098		
	tcacttaata atcaacctgg gggtcgaaat cagtgaagacc tggattcaaa ttctgccttg	1158		
	aaatattgtg actctgggaa tgacaacacc tggtttgttc tctgttgat cccagcccc	1218		
	aaagacagct cctggccata tatcaaggtt tcaataaata ttgctaaat gaaaaaaaaa	1278		
25	aaaaaaaaa aaaaaaaaaa aaa	1301		

<210> 2

<211> 282

<212> PRT

5 <213> human

<400> 2

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-50

-45

-40

10 Leu Thr Ala Ala Lys Glu Pro Gly Ala Arg Ser Ser Pro Leu Gln Ala Met

-35

-30

-25

Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu Val Gly Gly

-20

-15

-10

-5

Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro His Ser Gln Pro Trp

15

-1 1

5

10

Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly Ala Thr Leu Ile

15

20

25

30

Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu Lys Pro Arg Tyr Ile

35

40

45

20 Val His Leu Gly Gln His Asn Leu Gln Lys Glu Glu Gly Cys Glu Gln Thr

50

55

60

65

Arg Thr Ala Thr Glu Ser Phe Pro His Pro Gly Phe Asn Asn Ser Leu Pro

70

75

80

Asn Lys Asp His Arg Asn Asp Ile Met Leu Val Lys Met Ala Ser Pro Val

25

85

90

95

Ser Ile Thr Trp Ala Val Arg Pro Leu Thr Leu Ser Ser Arg Cys Val Thr  
 100                      105                      110                      115  
 Ala Gly Thr Ser Cys Leu Ile Ser Gly Trp Gly Ser Thr Ser Ser Pro Gln  
                          120                      125                      130  
 5    Leu Arg Leu Pro His Thr Leu Arg Cys Ala Asn Ile Thr Ile Ile Glu His  
                          135                      140                      145                      150  
 Gln Lys Cys Glu Asn Ala Tyr Pro Gly Asn Ile Thr Asp Thr Met Val Cys  
                          155                      160                      165  
 Ala Ser Val Gln Glu Gly Gly Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly  
 10                      170                      175                      180  
 Pro Leu Val Cys Asn Gln Ser Leu Gln Gly Ile Ile Ser Trp Gly Gln Asp  
 185                      190                      195                      200  
 Pro Cys Ala Ile Thr Arg Lys Pro Gly Val Tyr Thr Lys Val Cys Lys Tyr  
                          205                      210                      215  
 15    Val Asp Trp Ile Gln Glu Thr Met Lys Asn Asn  
                          220                      225  
  
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 <211> 1323  
 20    <212> DNA  
       <213> mouse  
  
 <400> 3  
 ccacatctga ctagggaagt aaggcgaagg aggcccatgg aagaaaaatc taaatgaaaa    60  
 25    cataagctag gagaactgag gcttcaaacc tgaagctatc ta atg agg agg ctg aag    117

Met Arg Arg Leu Lys

-45

agt gac tgg aaa tta tct aca gaa acc agg gaa cct ggc gcc cgc cct gcc 168

Ser Asp Trp Lys Leu Ser Thr Glu Thr Arg Glu Pro Gly Ala Arg Pro Ala

5

-40

-35

-30

cta ctc cag gcc agg atg att ctc cga ctc att gca ctt gct ctg gta aca 219

Leu Leu Gln Ala Arg Met Ile Leu Arg Leu Ile Ala Leu Ala Leu Val Thr

-25

-20

-15

-10

ggg cac gta ggg gga gag acg agg atc atc aag ggt tat gag tgc agg cct 270

10

Gly His Val Gly Gly Glu Thr Arg Ile Ile Lys Gly Tyr Glu Cys Arg Pro

-5

-1 1

5

cac tca cag cca tgg cag gtg gcc ctc ttt cag aag aca cgg ctt ctc tgt 321

His Ser Gln Pro Trp Gln Val Ala Leu Phe Gln Lys Thr Arg Leu Leu Cys

10

15

20

25

15

ggg gca acc ctc atc gcc ccc aaa tgg ctc ctg aca gca gcc cac tgc cgc 372

Gly Ala Thr Leu Ile Ala Pro Lys Trp Leu Leu Thr Ala Ala His Cys Arg

30

35

40

aag ccc cat tac gtg atc ctc ctt gga gag cac aat cta gag aag aca gac 423

Lys Pro His Tyr Val Ile Leu Leu Gly Glu His Asn Leu Glu Lys Thr Asp

20

45

50

55

60

ggc tgt gag cag agg cgg atg gcc act gag tcc ttc ccc cac ccc gac ttc 474

Gly Cys Glu Gln Arg Arg Met Ala Thr Glu Ser Phe Pro His Pro Asp Phe

65

70

75

aac aac agc ctc ccc aac aaa gac cac cgg aat gac ata atg ctt gtg aag 525

25

Asn Asn Ser Leu Pro Asn Lys Asp His Arg Asn Asp Ile Met Leu Val Lys

	80	85	90	
	atg tgc tct ccc gtc ttc ttt acc cga gct gtg cag cca ctc acc ctg tcc 576			
	Met Ser Ser Pro Val Phe Phe Thr Arg Ala Val Gln Pro Leu Thr Leu Ser			
	95	100	105	110
5	cca cac tgt gtc gct gca ggc acc agc tgc ctc att tct gga tgg ggc acc 627			
	Pro His Cys Val Ala Ala Gly Thr Ser Cys Leu Ile Ser Gly Trp Gly Thr			
	115	120	125	
	acg tcc agc ccc cag ttg cgc ctg cct cat tcc ttg cga tgt gcc aat gtc 678			
	Thr Ser Ser Pro Gln Leu Arg Leu Pro His Ser Leu Arg Cys Ala Asn Val			
10	130	135	140	145
	tcc atc atc gaa cac aag gag tgt gag aag gcc tac ccg ggc aac atc aca 729			
	Ser Ile Ile Glu His Lys Glu Cys Glu Lys Ala Tyr Pro Gly Asn Ile Thr			
	150	155	160	
	gac acc atg ctg tgc gcc agt gtt cgg aaa gag ggc aag gac tcc tgt cag 780			
15	Asp Thr Met Leu Cys Ala Ser Val Arg Lys Glu Gly Lys Asp Ser Cys Gln			
	165	170	175	
	ggc gac tct gga ggc ccc ctg gtc tgc aac gga tct ctt caa ggc atc atc 831			
	Gly Asp Ser Gly Gly Pro Leu Val Cys Asn Gly Ser Leu Gln Gly Ile Ile			
	180	185	190	195
20	tcc tgg ggt cag gac cca tgt gcc gtc acc aga aag cct ggt gtc tat aca 882			
	Ser Trp Gly Gln Asp Pro Cys Ala Val Thr Arg Lys Pro Gly Val Tyr Thr			
	200	205	210	
	aaa gtc tgc aaa tac ttt aac tgg atc cac gag gtt atg agg aac aat 930			
	Lys Val Cys Lys Tyr Phe Asn Trp Ile His Glu Val Met Arg Asn Asn			
25	215	220	225	

tagaggggac ctgcttccca ccaccaacc cctccaacct cttcttaatg ctttgacttc 990  
 tcttcattct gccctaagaa gtctcagct gggaccctgg catgtactct ctccgaccca 1050  
 ccatgagtat agtataggga tgctctaact tgatgatcga cctggggcct ggaatcaaata 1110  
 cctgacttga actaaattgt gactctggac atgatcacca ctggttttgt ttgtttgggt 1170  
 5 gttttttgtt ttgtttgtt ttgttcccag ctttgaagac agtccctggc atatcccagg 1230  
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1323

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10 <211> 276

<212> PRT

<213> mouse

<400> 4

15 Met Arg Arg Leu Lys

-45

Ser Asp Trp Lys Leu Ser Thr Glu Thr Arg Glu Pro Gly Ala Arg Pro Ala

-40

-35

-30

Leu Leu Gln Ala Arg Met Ile Leu Arg Leu Ile Ala Leu Ala Leu Val Thr

20

-25

-20

-15

-10

Gly His Val Gly Gly Glu Thr Arg Ile Ile Lys Gly Tyr Glu Cys Arg Pro

-5

-1 1

5

His Ser Gln Pro Trp Gln Val Ala Leu Phe Gln Lys Thr Arg Leu Leu Cys

10

15

20

25

25 Gly Ala Thr Leu Ile Ala Pro Lys Trp Leu Leu Thr Ala Ala His Cys Arg



	30	35	40
	Lys Pro His Tyr Val Ile Leu Leu Gly Glu His Asn Leu Glu Lys Thr Asp		
	45	50	55 60
	Gly Cys Glu Gln Arg Arg Met Ala Thr Glu Ser Phe Pro His Pro Asp Phe		
5	65	70	75
	Asn Asn Ser Leu Pro Asn Lys Asp His Arg Asn Asp Ile Met Leu Val Lys		
	80	85	90
	Met Ser Ser Pro Val Phe Phe Thr Arg Ala Val Gln Pro Leu Thr Leu Ser		
	95	100	105 110
10	Pro His Cys Val Ala Ala Gly Thr Ser Cys Leu Ile Ser Gly Trp Gly Thr		
	115	120	125
	Thr Ser Ser Pro Gln Leu Arg Leu Pro His Ser Leu Arg Cys Ala Asn Val		
	130	135	140 145
	Ser Ile Ile Glu His Lys Glu Cys Glu Lys Ala Tyr Pro Gly Asn Ile Thr		
15	150	155	160
	Asp Thr Met Leu Cys Ala Ser Val Arg Lys Glu Gly Lys Asp Ser Cys Gln		
	165	170	175
	Gly Asp Ser Gly Gly Pro Leu Val Cys Asn Gly Ser Leu Gln Gly Ile Ile		
	180	185	190 195
20	Ser Trp Gly Gln Asp Pro Cys Ala Val Thr Arg Lys Pro Gly Val Tyr Thr		
	200	205	210
	Lys Val Cys Lys Tyr Phe Asn Trp Ile His Glu Val Met Arg Asn Asn		
	215	220	225
25	<210> 5		

&lt;211&gt; 934

&lt;212&gt; DNA

&lt;213&gt; human

5 &lt;400&gt; 5

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atg agg att ctg cag tta atc ctg ctt gct ctg gca aca ggg ctt gta ggg 101

Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu Val Gly

10 -20 -15 -10 -5

gga gag acc agg atc atc aag ggg ttc gag tgc aag cct cac tcc cag ccc 152

Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro His Ser Gln Pro

-1 1 5 10

tgg cag gca gcc ctg ttc gag aag acg cgg cta ctc tgt ggg gcg acg ctc 203

15 Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly Ala Thr Leu

15 20 25 30

atc gcc ccc aga tgg ctc ctg aca gca gcc cac tgc ctc aag ccg tgg gtg 254

Ile Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu Lys Pro Trp Val

35 40 45

20 tca ctc acc tct ccc acc cat gtc tcc ccc gac ctt tcc tcc tcc aac tac 305

Ser Leu Thr Ser Pro Thr His Val Ser Pro Asp Leu Ser Ser Ser Asn Tyr

50 55 60

tgt ctc tcc cac ctc agc cgc tac ata gtt cac ctg ggg cag cac aac ctc 356

Cys Leu Ser His Leu Ser Arg Tyr Ile Val His Leu Gly Gln His Asn Leu

25 65 70 75 80

cag aag gag gag ggc tgt gag cag acc cgg aca gcc act gag tcc ttc ccc 407  
 Gln Lys Glu Glu Gly Cys Glu Gln Thr Arg Thr Ala Thr Glu Ser Phe Pro  
 85 90 95  
 cac ccc ggc ttc aac aac agc ctc ccc aac aaa gac cac cgc aat gac atc 458  
 5 His Pro Gly Phe Asn Asn Ser Leu Pro Asn Lys Asp His Arg Asn Asp Ile  
 100 105 110 115  
 atg ctg gtg aag atg gca tgc cca gtc tcc atc acc tgg gct gtg cga ccc 509  
 Met Leu Val Lys Met Ala Ser Pro Val Ser Ile Thr Trp Ala Val Arg Pro  
 120 125 130  
 10 ctc acc ctc tcc tca cgc tgy gtc act gct ggc acc agc tgc ctc att tcc 560  
 Leu Thr Leu Ser Ser Arg Cys Val Thr Ala Gly Thr Ser Cys Leu Ile Ser  
 135 140 145  
 ggc tgg ggc agc acg tcc agc ccc cag tta cgc ctg cct cac acc ttg cga 611  
 Gly Trp Gly Ser Thr Ser Ser Pro Gln Leu Arg Leu Pro His Thr Leu Arg  
 15 150 155 160 165  
 tgc gcc aac atc acc atc att gag cac cag aag tgt gag aac gcc tac ccc 662  
 Cys Ala Asn Ile Thr Ile Ile Glu His Gln Lys Cys Glu Asn Ala Tyr Pro  
 170 175 180  
 ggc aac atc aca gac acc atg gtg tgt gcc agc gtg cag gaa ggg ggc aag 713  
 20 Gly Asn Ile Thr Asp Thr Met Val Cys Ala Ser Val Gln Glu Gly Gly Lys  
 185 190 195 200  
 gac tcc tgc cag ggt gac tcc ggg ggc cct ctg gtc tgt aac cag tct ctt 764  
 Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Asn Gln Ser Leu  
 205 210 215  
 25 caa ggc att atc tcc tgg ggc cag gat ccg tgt gcg atc acc cga aag cct 815

Gln Gly Ile Ile Ser Trp Gly Gln Asp Pro Cys Ala Ile Thr Arg Lys Pro

220

225

230

ggt gtc tac acg aaa gtc tgc aaa tat gtg gac tgg atc cag gag acg atg 866

Gly Val Tyr Thr Lys Val Cys Lys Tyr Val Asp Trp Ile Gln Glu Thr Met

5

235

240

245

250

aag aac aat tagactggac ccaccaccca cagcccatca ccctccattt ccacttggtg 925

Lys Asn Asn

tttggttcc

934

10

<210> 6

<211> 275

<212> PRT

<213> human

15

<400> 6

Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu Val Gly

-20

-15

-10

-5

Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro His Ser Gln Pro

20

-1 1

5

10

Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly Ala Thr Leu

15

20

25

30

Ile Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu Lys Pro Trp Val

35

40

45

25

Ser Leu Thr Ser Pro Thr His Val Ser Pro Asp Leu Ser Ser Ser Asn Tyr

	50	55	60	
	Cys	Leu	Ser	His
	Leu	Ser	Arg	Tyr
	Ile	Val	His	Leu
	Gly	Gln	His	Asn
	Leu			
65		70	75	80
	Gln	Lys	Glu	Glu
	Gly	Cys	Glu	Gln
	Thr	Arg	Thr	Ala
	Thr	Glu	Ser	Phe
	Pro			
5	85	90	95	
	His	Pro	Gly	Phe
	Asn	Asn	Ser	Leu
	Pro	Asn	Lys	Asp
	His	Arg	Asn	Asp
	Ile			
	100	105	110	115
	Met	Leu	Val	Lys
	Met	Ala	Ser	Pro
	Val	Ser	Ile	Thr
	Trp	Ala	Val	Arg
	Pro			
	120	125	130	
10	Leu	Thr	Leu	Ser
	Ser	Arg	Cys	Val
	Thr	Ala	Gly	Thr
	Ser	Cys	Leu	Ile
	Ser			
	135	140	145	
	Gly	Trp	Gly	Ser
	Thr	Ser	Ser	Pro
	Gln	Leu	Arg	Leu
	Pro	His	Thr	Leu
	Arg			
	150	155	160	165
	Cys	Ala	Asn	Ile
	Thr	Ile	Ile	Glu
	His	Gln	Lys	Cys
	Glu	Asn	Ala	Tyr
	Pro			
15	170	175	180	
	Gly	Asn	Ile	Thr
	Asp	Thr	Met	Val
	Cys	Ala	Ser	Val
	Gln	Glu	Gly	Gly
	Lys			
	185	190	195	200
	Asp	Ser	Cys	Gln
	Gly	Asp	Ser	Gly
	Gly	Pro	Leu	Val
	Cys	Asn	Gln	Ser
	Leu			
	205	210	215	
20	Gln	Gly	Ile	Ile
	Ser	Trp	Gly	Gln
	Asp	Pro	Cys	Ala
	Ile	Thr	Arg	Lys
	Pro			
	220	225	230	
	Gly	Val	Tyr	Thr
	Lys	Val	Cys	Lys
	Tyr	Val	Asp	Trp
	Ile	Gln	Glu	Thr
	Met			
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	Lys	Asn	Asn	

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<211> 99

<212> DNA

<213> Artificial Sequence

5 <220>

<223> Designed oligonucleotide to construct plasmid pSecTrypHis

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aagcttggct agcaacacca tgaatctact cctgatacctt acctttgttg ctgctgctgt 60

10 tgctgcccc tttgacgacg atgacaagga tccgaattc 99

<210> 8

<211> 99

<212> DNA

15 <213> Artificial Sequence

<220>

<223> Designed oligonucleotide to construct plasmid pSecTrypHis

<400> 8

20 gaattcggat ccttgatcgc gtcgtcaaag ggggcagcaa cagcagcagc aacaaaggta 60

aggatcagga gtagattcat ggtgttgcta gccaaagctt 99

<210> 9

<211> 15

25 <212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to amplify neurosin-encoding sequence

5 <400> 9

ttggtgcatg gcgga

15

<210> 10

<211> 27

10 <212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to amplify neurosin-encoding sequence

15 <400> 10

tcctcgagac ttggcctgaa tggtttt

27

<210> 11

<211> 35

20 <212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to amplify a portion of plasmid  
pSecTrypHis/Neurosin

25

<400> 11

gcgctagcag atctccatga atctactcct gatcc

35

<210> 12

5 <211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to amplify a portion of plasmid

10 pSecTrypHis/Neurosin

<400> 12

tgaagcttgc catggaccaa cttgtcatc

29

15 <210> 13

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

20 <223> Designed oligonucleotide primer to amplify a portion of plasmid pTrypHis

<400> 13

ccaagcttca ccatcaccat caccat

26

25 <210> 14



<211> 17

<212> DNA

<213> Artificial Sequence

<220>

5     <223> Designed oligonucleotide primer to amplify a portion of plasmid  
pTrypSigTag

<400> 14

gcacagtcga ggctgat

17

10

<210> 15

<211> 17

<212> DNA

<213> Artificial Sequence

15     <220>

<223> Designed oligonucleotide primer to amplify a portion of plasmid  
pFBTrypSigTag

<400> 15

20     caaatgtggt atggctg

17

<210> 16

<211> 20

<212> DNA

25     <213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to amplify active hBSSP6-encoding sequence

<400> 16

5 atcatcaagg gttatgagtg

20

<210> 17

<211> 28

<212> DNA

10 <213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to amplify active hBSSP6-encoding sequence

<400> 17

15 cggaattcgc attaagaaga ggttgag

28

<210> 18

<211> 20

<212> DNA

20 <213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer designated as hBSSP6F1 for RACE for human  
BSSP6 (forward)

25 <400> 18

tcaagcccccg ctacatagtt

20

<210> 19

<211> 20

5 <212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer designated as hBSSP6F2 for RACE for human  
BSSP6 (forward)

10

<400> 19

atcatgctgg tgaagatggc

20

<210> 20

15 <211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer designated as hBSSP6F3 to amplify full-  
length human brain BSSP6-encoding mRNA (forward)

20

<400> 20

ggactcaaga gaggaacctg

20

25 <210> 21

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

5 <223> Designed oligonucleotide primer designated as hBSSP6F4 to amplify mature  
human BSSP6-encoding region (forward)

<400> 21

atcatcaagg ggttcgagtg

20

10

<210> 22

<211> 20

<212> DNA

<213> Artificial Sequence

15 <220>

<223> Designed oligonucleotide primer designated as hBSSP6F5 to amplify full-  
length human prostate BSSP6-encoding mRNA (forward)

<400> 22

20 ctgccttgct ccacacctgg

20

<210> 23

<211> 20

<212> DNA

25 <213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer designated as hBSSP6R1 for RACE for human  
BSSP6 (reverse)

5 <400> 23

ttctcacact tctggtgctc

20

<210> 24

<211> 20

10 <212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer designated as hBSSP6R2 for RACE for human  
BSSP6 (reverse)

15

<400> 24

atggtgtctg tgatgttgcc

20

<210> 25

20 <211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer designated as hBSSP6R3/P to amplify full-  
length human BSSP6-encoding mRNA (reverse)

25

<400> 25

aactgcagga accaaacacc aagtgg

26

5 <210> 26

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

10 <223> Designed oligonucleotide primer designated as mBSSP6F1 for RACE for mouse  
BSSP6 (forward)

<400> 26

cgacttcaac aacagcctcc

20

15

<210> 27

<211> 20

<212> DNA

<213> Artificial Sequence

20 <220>

<223> Designed oligonucleotide primer designated as mBSSP6F2 for RACE for mouse  
BSSP6 (forward)

<400> 27

25 cttctttacc cgagctgtgc

20

<210> 28

<211> 20

<212> DNA

5 <213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer designated as mBSSP6F3 to amplify full-length mouse prostate BSSP6-encoding mRNA (forward)

10 <400> 28

taagctagga gaactgaggc

20

<210> 29

<211> 18

15 <212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer designated as mBSSP6F4 to amplify mature mouse BSSP6-encoding region (forward)

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<400> 29

atcaagggtt atgagtgc

18

<210> 30

25 <211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer designated as mBSSP6F5 to amplify full-  
5 length mouse brain BSSP6-encoding mRNA (forward)

<400> 30

cttacaggct tggggattg

19

10 <210> 31

<211>

<212> DNA

<213> Artificial Sequence

<220> 20

15 <223> Designed oligonucleotide primer designated as mBSSP6R1 for RACE for mouse  
BSSP6 (reverse)

<400> 31

gatgatgcct tgaagagatc

20

20

<210> 32

<211> 21

<212> DNA

<213> Artificial Sequence

25 <220>



<223> Designed oligonucleotide primer designated as mBSSP6R2 for RACE for mouse BSSP6 (reverse)

<400> 32

5 catggtgtct gtgatgttgc c

21

<210> 33

<211> 28

<212> DNA

10 <213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer designated as mBSSP6R3/E to amplify full-length mouse BSSP6-encoding mRNA (reverse)

15 <400> 33

cggaattcgc attaagaaga ggttggag

28

<210> 34

<211> 20

20 <212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer designated as hBSSP6R3 to amplify a portion of BSSP6 variant type-encoding mRNA from human prostatic cancer cell

25 line PC-3 (reverse)

<400> 34

atggtgtctg tgatgttgcc

20

5 <210> 35

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

10 <223> Designed oligonucleotide primer designated as hBSSP6F7 to amplify a  
portion of human BSSP6-encoding mRNA (forward)

<400> 35

cctcaagccg tgggtgtcac

20

15

<210> 36

<211> 20

<212> DNA

<213> Artificial Sequence

20 <220>

<223> Designed oligonucleotide primer to amplify conserved region of serin  
proteases-encoding sequence

<220>

<221> UNSURE

25 <222> 9, 12

<223> n is a, c, g or t.

<400> 36

gtgctcacng cngcbcaytg

20

5

<210> 37

<211> 20

<212> DNA

<213> Artificial Sequence

10

<220>

<223> Designed oligonucleotide primer to amplify conserved region of serin  
proteases-encoding sequence

<220>

<221> UNSURE

15

<222> 12, 15

<223> n is a, c, g or t.

<400> 37

ccvctrwsdc cncnggcga

20

20

<210> 38

<211> 117

<212> DNA

<213> Artificial Sequence

25

<220>

<223> Designed oligonucleotide to construct plasmid pTrypHis

<400> 38

AAGCTTGGCT AGCAACACCA TGAATCTACT CCTGATCCTT ACCTTTGTTG CTGCTGCTGT 60

5 TGCTGCCCCG TTTCACCATC ACCATCACCA TGACGACGAT GACAAGGATC CGAATTC 117

<210> 39

<211> 117

<212> DNA

10 <213> Artificial Sequence

<220>

<223> Designed oligonucleotide to construct plasmid pTrypHis

<400> 39

15 GAATTCGGAT CCTGTGCATC GTCGTCATGG TGATGGTGAT GGTGAAAGGG GGCAGCAACA 60

GCAGCAGCAA CAAAGGTAAG GATCAGGAGT AGATTCATGG TGTGCTAGC CAAGCTT 117

Subcl